

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/529,512
Source: PCF
Date Processed by STIC: 7/10/06

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/529,512

DATE: 07/10/2006

TIME: 10:21:22

Input Set : A:\BER03US1.APP

Output Set: N:\CRF4\07102006\J529512.raw

3 <110> APPLICANT: WHITE, JOHN
 4 FERNANDES, ISABELLE
 6 <120> TITLE OF INVENTION: NUCLEAR RECEPTOR TRANSCRIPTIONAL COREPRESSOR AND USES
 7 THEREOF
 9 <130> FILE REFERENCE: BER-003US1
 11 <140> CURRENT APPLICATION NUMBER: 10/529,512
 12 <141> CURRENT FILING DATE: 2005-03-25
 14 <150> PRIOR APPLICATION NUMBER: PCT/CA03/01477
 15 <151> PRIOR FILING DATE: 2003-09-25
 17 <150> PRIOR APPLICATION NUMBER: 60/413,602
 18 <151> PRIOR FILING DATE: 2002-09-26
 20 <160> NUMBER OF SEQ ID NOS: 30
 22 <170> SOFTWARE: PatentIn Ver. 3.3
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1828
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (527)..(1825)
 33 <400> SEQUENCE: 1

34 ccacgacaac ccactgcaag cagatccagc agctgcttcc tgtaatgcag gactccccag 60
 36 gagcaccag gcatgggcag caaccctgc atgccattct ttttgggctc ccgagaacag 120
 38 ggagataaac accaccatca tctgagagcc ggggaagggga aggcgagggg gtgtaggcgg 180
 40 cacgaatgct ccgttgagag acgcggcttt cggcaagaac tggattcgtg gcgccacaag 240
 42 ctcatctact gtgtaggtcc cgtttccctc tgtgcggcgg ccggcgggac cataagggct 300
 44 taactcatat atttaacccc cctccaaaaa ggtttgaaag tattcttgaa gggctgtttg 360
 46 gacctgcatt attaaaagat ctcaagttat ttaaagactg tgaacctgaa agcatttctg 420
 48 attggacttt tgatgaaaac tgtttattct gttgcttgag aagagataaa gtaaagacag 480
 50 tccctgggctc tccgaccca atattccct agtggcccg gagatc atg cag cga 535
 51 Met Gln Arg
 52 1
 54 atg atc caa caa ttt gct gct gaa tat acc tca aaa aat agc tct act 583
 55 Met Ile Gln Gln Phe Ala Ala Glu Tyr Thr Ser Lys Asn Ser Ser Thr
 56 5 10 15
 58 cag gac ccc agc cag ccc aat agc aca aag aac caa agc ctg ccg aaa 631
 59 Gln Asp Pro Ser Gln Pro Asn Ser Thr Lys Asn Gln Ser Leu Pro Lys
 60 20 25 30 35
 62 gca tct cca gtc acc acc tct ccc acg gct gca act act cag aac cct 679
 63 Ala Ser Pro Val Thr Thr Ser Pro Thr Ala Ala Thr Thr Gln Asn Pro
 64 40 45 50
 66 gtg ctc agc aaa ctt ctc atg gct gac caa gac tca cct ctg gac ctt 727
 67 Val Leu Ser Lys Leu Leu Met Ala Asp Gln Asp Ser Pro Leu Asp Leu

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68		55		60		65		
70	act	gtc	aga	aag	tct	cag	tca	gaa cct agc gaa caa gac ggt gta ctt 775
71	Thr	Val	Arg	Lys	Ser	Gln	Ser	Glu Pro Ser Glu Gln Asp Gly Val Leu
72			70			75		80
74	gat	ctg	tcc	act	aag	aaa	agt	cca tgt gct ggc agc act tcc ctg agc 823
75	Asp	Leu	Ser	Thr	Lys	Lys	Ser	Pro Cys Ala Gly Ser Thr Ser Leu Ser
76		85				90		95
78	cac	tct	cca	ggc	tgc	tcc	agt	act caa ggg aac ggg cga cct ggg aga 871
79	His	Ser	Pro	Gly	Cys	Ser	Ser	Thr Gln Gly Asn Gly Arg Pro Gly Arg
80	100				105			110 115
82	ccc	agc	cag	tac	cgc	cca	gac	gga ctt cgg agt ggt gat ggg gta cct 919
83	Pro	Ser	Gln	Tyr	Arg	Pro	Asp	Gly Leu Arg Ser Gly Asp Gly Val Pro
84				120			125	130
86	cca	aga	agc	tta	cag	gat	gga	acc agg gaa ggt ttt gga cac tcc aca 967
87	Pro	Arg	Ser	Leu	Gln	Asp	Gly	Thr Arg Glu Gly Phe Gly His Ser Thr
88			135			140		145
90	tca	ctc	aaa	gtt	cca	ctg	gct	cga tcc ctg cag att agt gaa gaa cta 1015
91	Ser	Leu	Lys	Val	Pro	Leu	Ala	Arg Ser Leu Gln Ile Ser Glu Glu Leu
92			150			155		160
94	ctg	agc	aga	aac	caa	ttg	tcc	aca gct gcc agc ctt ggg cca tct gga 1063
95	Leu	Ser	Arg	Asn	Gln	Leu	Ser	Thr Ala Ala Ser Leu Gly Pro Ser Gly
96		165				170		175
98	tta	cag	aat	cat	gga	caa	cac	tta ata tta tcc agg gaa gcc tct tgg 1111
99	Leu	Gln	Asn	His	Gly	Gln	His	Leu Ile Leu Ser Arg Glu Ala Ser Trp
100	180				185			190 195
102	gca	aaa	cca	cat	tac	gag	ttc	aac ctc agc cgt atg aag ttc agg gga 1159
103	Ala	Lys	Pro	His	Tyr	Glu	Phe	Asn Leu Ser Arg Met Lys Phe Arg Gly
104				200			205	210
106	aat	ggt	gca	ctc	agc	aac	atc	agt gac ctt cct ttt ctt gca gaa aac 1207
107	Asn	Gly	Ala	Leu	Ser	Asn	Ile	Ser Asp Leu Pro Phe Leu Ala Glu Asn
108			215			220		225
110	tct	gcc	ttt	cca	aaa	atg	gca	ctt caa gca aaa caa gat gga aaa aag 1255
111	Ser	Ala	Phe	Pro	Lys	Met	Ala	Leu Gln Ala Lys Gln Asp Gly Lys Lys
112			230			235		240
114	gac	gtg	agc	cat	tca	tct	cct	gta gat tta aag ata cca caa gtt cga 1303
115	Asp	Val	Ser	His	Ser	Ser	Pro	Val Asp Leu Lys Ile Pro Gln Val Arg
116		245				250		255
118	gga	atg	gat	ctt	tct	tgg	gag	tct cgc act ggt gat cag tac agc tat 1351
119	Gly	Met	Asp	Leu	Ser	Trp	Glu	Ser Arg Thr Gly Asp Gln Tyr Ser Tyr
120	260				265			270 275
122	agc	tct	ttg	gta	atg	ggc	tca	caa acg gag agc gcg ctt agt aaa aaa 1399
123	Ser	Ser	Leu	Val	Met	Gly	Ser	Gln Thr Glu Ser Ala Leu Ser Lys Lys
124				280			285	290
126	tta	agg	gct	att	ctt	cca	aaa	caa agt aga aaa agc atg tta gat gct 1447
127	Leu	Arg	Ala	Ile	Leu	Pro	Lys	Gln Ser Arg Lys Ser Met Leu Asp Ala
128			295			300		305
130	ggg	ccc	gat	tct	tgg	ggc	tca	gat gct gag cag tct acc cct gga cag 1495
131	Gly	Pro	Asp	Ser	Trp	Gly	Ser	Asp Ala Glu Gln Ser Thr Pro Gly Gln
132			310			315		320

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134 cca tat ccc aca tcg gat caa gaa gga gac cct ggc tcc aag cag cct 1543
135 Pro Tyr Pro Thr Ser Asp Gln Glu Gly Asp Pro Gly Ser Lys Gln Pro
136      325      330      335
138 cgg aag aaa aga ggg cgt tac aga cag tac aac agt gag ata ctg gag 1591
139 Arg Lys Lys Arg Gly Arg Tyr Arg Gln Tyr Asn Ser Glu Ile Leu Glu
140 340      345      350      355
142 gaa gca atc tca gtg gtt atg agt gga aaa atg agt gtt tcc aaa gct 1639
143 Glu Ala Ile Ser Val Val Met Ser Gly Lys Met Ser Val Ser Lys Ala
144      360      365      370
146 cag agt att tat ggg att ccc cac agt aca ctg gag tac aaa gta aag 1687
147 Gln Ser Ile Tyr Gly Ile Pro His Ser Thr Leu Glu Tyr Lys Val Lys
148      375      380      385
150 gag agg ctg ggc act ttg aaa aac cct cca aag aaa aag atg aaa tta 1735
151 Glu Arg Leu Gly Thr Leu Lys Asn Pro Pro Lys Lys Lys Met Lys Leu
152      390      395      400
154 atg agg tcg gag ggg cca gat gtt tct gta aag att gaa tta gat ccc 1783
155 Met Arg Ser Glu Gly Pro Asp Val Ser Val Lys Ile Glu Leu Asp Pro
156      405      410      415
158 cag gga gag gca gca caa agt gca aat gaa tca aaa aac gag tag 1828
159 Gln Gly Glu Ala Ala Gln Ser Ala Asn Glu Ser Lys Asn Glu
160 420      425      430
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 433
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 2
169 Met Gln Arg Met Ile Gln Gln Phe Ala Ala Glu Tyr Thr Ser Lys Asn
170 1 5 10 15
172 Ser Ser Thr Gln Asp Pro Ser Gln Pro Asn Ser Thr Lys Asn Gln Ser
173 20 25 30
175 Leu Pro Lys Ala Ser Pro Val Thr Thr Ser Pro Thr Ala Ala Thr Thr
176 35 40 45
178 Gln Asn Pro Val Leu Ser Lys Leu Leu Met Ala Asp Gln Asp Ser Pro
179 50 55 60
181 Leu Asp Leu Thr Val Arg Lys Ser Gln Ser Glu Pro Ser Glu Gln Asp
182 65 70 75 80
184 Gly Val Leu Asp Leu Ser Thr Lys Lys Ser Pro Cys Ala Gly Ser Thr
185 85 90 95
187 Ser Leu Ser His Ser Pro Gly Cys Ser Ser Thr Gln Gly Asn Gly Arg
188 100 105 110
190 Pro Gly Arg Pro Ser Gln Tyr Arg Pro Asp Gly Leu Arg Ser Gly Asp
191 115 120 125
193 Gly Val Pro Pro Arg Ser Leu Gln Asp Gly Thr Arg Glu Gly Phe Gly
194 130 135 140
196 His Ser Thr Ser Leu Lys Val Pro Leu Ala Arg Ser Leu Gln Ile Ser
197 145 150 155 160
199 Glu Glu Leu Leu Ser Arg Asn Gln Leu Ser Thr Ala Ala Ser Leu Gly
200 165 170 175
202 Pro Ser Gly Leu Gln Asn His Gly Gln His Leu Ile Leu Ser Arg Glu

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```

203          180          185          190
205 Ala Ser Trp Ala Lys Pro His Tyr Glu Phe Asn Leu Ser Arg Met Lys
206          195          200          205
208 Phe Arg Gly Asn Gly Ala Leu Ser Asn Ile Ser Asp Leu Pro Phe Leu
209          210          215          220
211 Ala Glu Asn Ser Ala Phe Pro Lys Met Ala Leu Gln Ala Lys Gln Asp
212 225          230          235          240
214 Gly Lys Lys Asp Val Ser His Ser Ser Pro Val Asp Leu Lys Ile Pro
215          245          250          255
217 Gln Val Arg Gly Met Asp Leu Ser Trp Glu Ser Arg Thr Gly Asp Gln
218          260          265          270
220 Tyr Ser Tyr Ser Ser Leu Val Met Gly Ser Gln Thr Glu Ser Ala Leu
221          275          280          285
223 Ser Lys Lys Leu Arg Ala Ile Leu Pro Lys Gln Ser Arg Lys Ser Met
224          290          295          300
226 Leu Asp Ala Gly Pro Asp Ser Trp Gly Ser Asp Ala Glu Gln Ser Thr
227 305          310          315          320
229 Pro Gly Gln Pro Tyr Pro Thr Ser Asp Gln Glu Gly Asp Pro Gly Ser
230          325          330          335
232 Lys Gln Pro Arg Lys Lys Arg Gly Arg Tyr Arg Gln Tyr Asn Ser Glu
233          340          345          350
235 Ile Leu Glu Glu Ala Ile Ser Val Val Met Ser Gly Lys Met Ser Val
236          355          360          365
238 Ser Lys Ala Gln Ser Ile Tyr Gly Ile Pro His Ser Thr Leu Glu Tyr
239          370          375          380
241 Lys Val Lys Glu Arg Leu Gly Thr Leu Lys Asn Pro Pro Lys Lys Lys
242 385          390          395          400
244 Met Lys Leu Met Arg Ser Glu Gly Pro Asp Val Ser Val Lys Ile Glu
245          405          410          415
247 Leu Asp Pro Gln Gly Glu Ala Ala Gln Ser Ala Asn Glu Ser Lys Asn
248          420          425          430
250 Glu
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 60
257 <212> TYPE: PRT
258 <213> ORGANISM: Homo sapiens
260 <400> SEQUENCE: 3
261 Lys Gln Pro Lys Lys Arg Gly Arg Tyr Arg Gln Tyr Asn Ser Glu
262 1          5          10          15
264 Ile Leu Glu Glu Ala Ile Ser Val Val Met Ser Gly Lys Met Ser Val
265          20          25          30
267 Ser Lys Ala Gln Ser Ile Tyr Gly Ile Pro His Ser Thr Leu Glu Tyr
268          35          40          45
270 Lys Val Lys Glu Arg Leu Gly Thr Leu Lys Asn Pro
271          50          55          60
274 <210> SEQ ID NO: 4
275 <211> LENGTH: 17
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial Sequence

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279 <220> FEATURE:
280 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
281     peptide
283 <400> SEQUENCE: 4
284 Gln Asp Pro Ser Gln Pro Asn Ser Thr Lys Asn Gln Ser Leu Pro Lys
285   1               5               10               15
287 Ala
291 <210> SEQ ID NO: 5
292 <211> LENGTH: 30
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
298     primer
300 <400> SEQUENCE: 5
301 ccggaattcc ggatgaccat gaccctccac                      30
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 31
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
311     primer
313 <400> SEQUENCE: 6
314 cgggatcccg tcaaaggtgg acctgatcat g                      31
317 <210> SEQ ID NO: 7
318 <211> LENGTH: 40
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
324     primer
326 <400> SEQUENCE: 7
327 ccggaattcc ggcccgggca tgagacagtc cctgggtctc          40
330 <210> SEQ ID NO: 8
331 <211> LENGTH: 20
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
337     primer
339 <400> SEQUENCE: 8
340 ttcttgaggg taccatca                      20
343 <210> SEQ ID NO: 9
344 <211> LENGTH: 30
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; Xaa Pos. 2,4,6,8

Seq#:21; Xaa Pos. 5,6,7

Seq#:22; Xaa Pos. 2,6,7

VERIFICATION SUMMARY

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L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0